

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: De Robertis, Edward M.
Bouwmeester, Tewis
- (ii) TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
Factors
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Majestic, Parsons, Siebert & Hsue
 - (B) STREET: Four Embarcadero Center, Suite 1100
 - (C) CITY: San Francisco
 - (D) STATE: California
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 94111-4106
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/878,474
 - (B) FILING DATE: 18-JUN-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/020,150
 - (B) FILING DATE: 20-JUN-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Siebert, J. Suzanne
 - (B) REGISTRATION NUMBER: 28,758
 - (C) REFERENCE/DOCKET NUMBER: 3100.002US1
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415/248-5500
 - (B) TELEFAX: 415/362-5418

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Leu Leu Asn Val Leu Arg Ile Cys Ile Ile Val Cys Leu Val Asn
1 5 10 15
Asp Gly Ala Gly Lys His Ser Glu Gly Arg Glu Arg Thr Lys Thr Tyr
20 25 30
Ser Leu Asn Ser Arg Gly Tyr Phe Arg Lys Glu Arg Gly Ala Arg Arg
35 40 45
Ser Lys Ile Leu Leu Val Asn Thr Lys Gly Leu Asp Glu Pro His Ile
50 55 60
Gly His Gly Asp Phe Gly Leu Val Ala Glu Leu Phe Asp Ser Thr Arg
65 70 75 80
Thr His Thr Asn Arg Lys Glu Pro Asp Met Asn Lys Val Lys Leu Phe
85 90 95
Ser Thr Val Ala His Gly Asn Lys Ser Ala Arg Arg Lys Ala Tyr Asn
100 105 110
Gly Ser Arg Arg Asn Ile Phe Ser Arg Arg Ser Phe Asp Lys Arg Asn
115 120 125
Thr Glu Val Thr Glu Lys Pro Gly Ala Lys Met Phe Trp Asn Asn Phe
130 135 140
Leu Val Lys Met Asn Gly Ala Pro Gln Asn Thr Ser His Gly Ser Lys
145 150 155 160
Ala Gln Glu Ile Met Lys Glu Ala Cys Lys Thr Leu Pro Phe Thr Gln
165 170 175
Asn Ile Val His Glu Asn Cys Asp Arg Met Val Ile Gln Asn Asn Leu
180 185 190
Cys Phe Gly Lys Cys Ile Ser Leu His Val Pro Asn Gln Gln Asp Arg
195 200 205
Arg Asn Thr Cys Ser His Cys Leu Pro Ser Lys Phe Thr Leu Asn His
210 215 220

Leu Thr Leu Asn Cys Thr Gly Ser Lys Asn Val Val Lys Val Val Met
225 230 235 240

Met Val Glu Glu Cys Thr Cys Glu Ala His Lys Ser Asn Phe His Gln
245 250 255

Thr Ala Gln Phe Asn Met Asp Thr Ser Thr Thr Leu His His
260 265 270

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCCTAA AAGCGGCACA GTGCAGGAAC AGCAAGTCGC TCAGAAACAC TGCAGGGTCT	60
AGATATCATA CAATGTTACT AAATGTACTC AGGATCTGTA TTATCGTCTG CCTTGTGAAT	120
GATGGAGCAG GAAAACACTC AGAAGGACGA GAAAGGACAA AAACATATTC ACTTAACAGC	180
AGAGGTTACT TCAGAAAAGA AAGAGGAGCA CGTAGGAGCA AGATTCTGCT GGTGAATACT	240
AAAGGTCTTG ATGAACCCCA CATTGGGCAT GGTGATTTTG GCTTAGTAGC TGAACTATTT	300
GATTCCACCA GAACACATAC AAACAGAAAA GAGCCAGACA TGAACAAAGT CAAGCTTTTC	360
TCAACAGTTG CCCATGGAAA CAAAAGTGCA AGAAGAAAAG CTTACAATGG TTCTAGAAGG	420
AATATTTTTT CTCGCCGTTT TTTTGATAAA AGAAATACAG AGGTTACTGA AAAGCCTGGT	480
GCCAAGATGT TCTGGAACAA TTTTTTGGTT AAAATGAATG GAGCCCCACA GAATACAAGC	540
CATGGCAGTA AAGCACAGGA AATAATGAAA GAAGCTTGCA AAACCTTGCC CTTCACTCAG	600
AATATTGTAC ATGAAAAC TGACAGGATG GTGATACAGA ACAATCTGTG CTTTGGTAAA	660
TGCATCTCTC TCCATGTTCC AAATCAGCAA GATCGACGAA ATACTTGTTT CCATTGCTTG	720
CCGTCCAAAT TTACCCTGAA CCACCTGACG CTGAATTGTA CTGGATCTAA GAATGTAGTA	780
AAGGTTGTCA TGATGGTAGA GGAATGCACG TGTGAAGCTC ATAAGAGCAA CTTCCACCAA	840

ACTGCACAGT TTAACATGGA TACATCTACT ACCCTGCACC ATTAAAAGGA CTGTCTGCCA 900
TACAGTATGG AAATGCCCCAT TTGTTGGAAT ATTCGTTACA TGCTATGTAT CTAAAGCATT 960
ATGTTGCCTT CTGTTTCATA TAACCACATG GAATAAGGAT TGTATGAATT ATAATTAACA 1020
AATGGCATT TGTGTAACAT GCAAGATCTC TGTTCATCA GTTGCAAGAT AAAAGGCAAT 1080
ATTTGTTTGA CTTTTTCTA CAAAATGAAT ACCCAAATAT ATGATAAGAT AATGGGGTCA 1140
AAACTGTTAA GGGGTAATGT AATAATAGGG ACTACAACC AATCAGCAGG TATGATTTAC 1200
TGGTCACCTG TTTAAAAGCA AACATCTTAT TGGTTGCTAT GGGTACTGC TTCTGGGCAA 1260
AATGTGTGCC TCATAGGGGG GTTAGTGTGT TGTGTACTGA ATTAATTGTA TTTATTTTCAT 1320
TGTTACAATG AAGAGGATGT CTATGTTTAT TTCACTTTTA TTAATGTACA ATAAATGTTC 1380
TTGTTTCTTT AAAAAAAAAA AAAAATCGA G 1411

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ser	Arg	Thr	Arg	Lys	Val	Asp	Ser	Leu	Leu	Leu	Leu	Ala	Ile	Pro
1				5					10					15	
Gly	Leu	Ala	Leu	Leu	Leu	Leu	Pro	Asn	Ala	Tyr	Cys	Ala	Ser	Cys	Glu
			20					25					30		
Pro	Val	Arg	Ile	Pro	Met	Cys	Lys	Ser	Met	Pro	Trp	Asn	Met	Thr	Lys
		35					40					45			
Met	Pro	Asn	His	Leu	His	His	Ser	Thr	Gln	Ala	Asn	Ala	Ile	Leu	Ala
	50					55					60				
Ile	Glu	Gln	Phe	Glu	Gly	Leu	Leu	Thr	Thr	Glu	Cys	Ser	Gln	Asp	Leu
65					70					75					80
Leu	Phe	Phe	Leu	Cys	Ala	Met	Tyr	Ala	Pro	Ile	Cys	Thr	Ile	Asp	Phe
			85						90					95	

Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys Glu Arg Ala Arg
 100 105 110
 Ala Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His Thr Trp Pro Glu
 115 120 125
 Ser Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg Gly Val Cys Ile
 130 135 140
 Ser Pro Glu Ala Ile Val Thr Val Glu Gln Gly Thr Asp Ser Met Pro
 145 150 155 160
 Asp Phe Ser Met Asp Ser Asn Asn Gly Asn Cys Gly Ser Gly Arg Glu
 165 170 175
 His Cys Lys Cys Lys Pro Met Lys Ala Thr Gln Lys Thr Tyr Leu Lys
 180 185 190
 Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Val Lys Val
 195 200 205
 Lys Cys His Asp Ala Thr Ala Ile Val Glu Val Lys Glu Ile Leu Lys
 210 215 220
 Ser Ser Leu Val Asn Ile Pro Lys Asp Thr Val Thr Leu Tyr Thr Asn
 225 230 235 240
 Ser Gly Cys Leu Cys Pro Gln Leu Val Ala Asn Glu Glu Tyr Ile Ile
 245 250 255
 Met Gly Tyr Glu Asp Lys Glu Arg Thr Arg Leu Leu Leu Val Glu Gly
 260 265 270
 Ser Leu Ala Glu Lys Trp Arg Asp Arg Leu Ala Lys Lys Val Lys Arg
 275 280 285
 Trp Asp Gln Lys Leu Arg Arg Pro Arg Lys Ser Lys Asp Pro Val Ala
 290 295 300
 Pro Ile Pro Asn Lys Asn Ser Asn Ser Arg Gln Ala Arg Ser
 305 310 315

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1875 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCCTT TCACACAGGA CTCCTGGCAG AGGTGAATGG TTAGCCCTAT GGATTTGGTT 60
TGTTGATTTT GACACATGAT TGATTGCTTT CAGATAGGAT TGAAGGACTT GGATTTTAT 120
CTAATTCTGC ACTTTTAAAT TATCTGAGTA ATTGTTTCATT TTGTATTGGA TGGGACTAAA 180
GATAAACTTA ACTCCTTGCT TTTGACTTGC CCATAAACTA TAAGGTGGGG TGAGTTGTAG 240
TTGCTTTTAC ATGTGCCCAG ATTTTCCCTG TATTCCCTGT ATTCCCTCTA AAGTAAGCCT 300
ACACATACAG GTTGGGCAGA ATAACAATGT CTCGAACAAG GAAAGTGGAC TCATTACTGC 360
TACTGGCCAT ACCTGGACTG GCGCTTCTCT TATTACCCAA TGCTTACTGT GCTTCGTGTG 420
AGCCTGTGCG GATCCCATG TGCAAATCTA TGCCATGGAA CATGACCAAG ATGCCCAACC 480
ATCTCCACCA CAGCACTCAA GCCAATGCCA TCCTGGCAAT TGAACAGTTT GAAGGTTTGC 540
TGACCACTGA ATGTAGCCAG GACCTTTTGT TCTTTCTGTG TGCCATGTAT GCCCCATTT 600
GTACCATCGA TTTCCAGCAT GAACCAATTA AGCCTTGCAA GTCCGTGTGC GAAAGGGCCA 660
GGGCCGGCTG TGAGCCCATT CTCATAAAGT ACCGGCACAC TTGGCCAGAG AGCCTGGCAT 720
GTGAAGAGCT GCCCGTATAT GACAGAGGAG TCTGCATCTC CCCAGAGGCT ATCGTCACAG 780
TGGAACAAGG AACAGATTCA ATGCCAGACT TCTCCATGGA TTCAAACAAT GGAAATTGCG 840
GAAGCGGCAG GGAGCACTGT AAATGCAAGC CCATGAAGGC AACCCAAAAG ACGTATCTCA 900
AGAATAATTA CAATTATGTA ATCAGAGCAA AAGTGAAAGA GGTGAAAGTG AAATGCCACG 960
ACGCAACAGC AATTGTGGAA GTAAAGGAGA TTCTCAAGTC TTCCCTAGTG AACATTCCTA 1020
AAGACACAGT GACACTGTAC ACCAACTCAG GCTGCTTGTG CCCCAGCTT GTTGCCAATG 1080
AGGAATACAT AATTATGGGC TATGAAGACA AAGAGCGTAC CAGGCTTCTA CTAGTGGAAG 1140
GATCCTTGGC CGAAAAATGG AGAGATCGTC TTGCTAAGAA AGTCAAGCGC TGGGATCAAA 1200
AGCTTCGACG TCCCAGGAAA AGCAAAGACC CCGTGGCTCC AATTCCCAAC AAAAACAGCA 1260
ATTCCAGACA AGCGCGTAGT TAGACTAACG GAAAGGTGTA TGGAAGTCT ATGGACTTTG 1320
AAACTAAGAT TTGCATTGTT GGAAGAGCAA AAAAGAAATT GCACTACAGC ACGTTATATT 1380
CTATTGTTTA CTACAAGAAG CTGGTTTAGT TGATTGTAGT TCTCCTTTCC TTCTTTTTTT 1440

TTATAACTAT ATTTGCACGT GTTCCCAGGC AATTGTTTTA TTCAACTTCC AGTGACAGAG 1500
 CAGTGACTGA ATGTCTCAGC CTAAAGAAGC TCAATTCATT TCTGATCAAC TAATGGTGAC 1560
 AAGTGTTTGA TACTTGGGGA AAGTGA ACTA ATTGCAATGG TAAATCAGAG AAAAGTTGAC 1620
 CAATGTTGCT TTTCTGTAG ATGAACAAGT GAGAGATCAC ATTTAAATGA TGATCACTTT 1680
 CCATTTAATA CTTTCAGCAG TTTTAGTTAG ATGACATGTA GGATGCACCT AAATCTAAAT 1740
 ATTTTATCAT AAATGAAGAG CTGGTTTAGA CTGTATGGTC ACTGTTGGGA AGGTAAATGC 1800
 CTACTTTGTC AATTCTGTTT TAAAAATTGC CTAAATAAAT ATTAAGTCCT AAATAAAAAA 1860
 AAAAAAAAAA AAAAA 1875

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 979 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Leu	Leu	Leu	Phe	Arg	Ala	Ile	Pro	Met	Leu	Leu	Leu	Gly	Leu	Met	1	5	10	15
Val	Leu	Gln	Thr	Asp	Cys	Glu	Ile	Ala	Gln	Tyr	Tyr	Ile	Asp	Glu	Glu	20	25	30	
Glu	Pro	Pro	Gly	Thr	Val	Ile	Ala	Val	Leu	Ser	Gln	His	Ser	Ile	Phe	35	40	45	
Asn	Thr	Thr	Asp	Ile	Pro	Ala	Thr	Asn	Phe	Arg	Leu	Met	Lys	Gln	Phe	50	55	60	
Asn	Asn	Ser	Leu	Ile	Gly	Val	Arg	Glu	Ser	Asp	Gly	Gln	Leu	Ser	Ile	65	70	75	80
Met	Glu	Arg	Ile	Asp	Arg	Glu	Gln	Ile	Cys	Arg	Gln	Ser	Leu	His	Cys	85	90	95	
Asn	Leu	Ala	Leu	Asp	Val	Val	Ser	Phe	Ser	Lys	Gly	His	Phe	Lys	Leu	100	105	110	

Leu	Asn	Val	Lys	Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	His	Ser	Pro	His
	115						120					125			
Phe	Pro	Ser	Glu	Ile	Met	His	Val	Glu	Val	Ser	Glu	Ser	Ser	Ser	Val
	130					135					140				
Gly	Thr	Arg	Ile	Pro	Leu	Glu	Ile	Ala	Ile	Asp	Glu	Asp	Val	Gly	Ser
145					150					155					160
Asn	Ser	Ile	Gln	Asn	Phe	Gln	Ile	Ser	Asn	Asn	Ser	His	Phe	Ser	Ile
				165					170					175	
Asp	Val	Leu	Thr	Arg	Ala	Asp	Gly	Val	Lys	Tyr	Ala	Asp	Leu	Val	Leu
			180					185					190		
Met	Arg	Glu	Leu	Asp	Arg	Glu	Ile	Gln	Pro	Thr	Tyr	Ile	Met	Glu	Leu
		195					200					205			
Leu	Ala	Met	Asp	Gly	Gly	Val	Pro	Ser	Leu	Ser	Gly	Thr	Ala	Val	Val
	210					215					220				
Asn	Ile	Arg	Val	Leu	Asp	Phe	Asn	Asp	Asn	Ser	Pro	Val	Phe	Glu	Arg
225					230					235					240
Ser	Thr	Ile	Ala	Val	Asp	Leu	Val	Glu	Asp	Ala	Pro	Leu	Gly	Tyr	Leu
				245					250					255	
Leu	Leu	Glu	Leu	His	Ala	Thr	Asp	Asp	Asp	Glu	Gly	Val	Asn	Gly	Glu
			260					265					270		
Ile	Val	Tyr	Gly	Phe	Ser	Thr	Leu	Ala	Ser	Gln	Glu	Val	Arg	Gln	Leu
		275					280					285			
Phe	Lys	Ile	Asn	Ser	Arg	Thr	Gly	Ser	Val	Thr	Leu	Glu	Gly	Gln	Val
	290					295					300				
Asp	Phe	Glu	Thr	Lys	Gln	Thr	Tyr	Glu	Phe	Glu	Val	Gln	Ala	Gln	Asp
305					310					315					320
Leu	Gly	Pro	Asn	Pro	Leu	Thr	Ala	Thr	Cys	Lys	Val	Thr	Val	His	Ile
				325					330					335	
Leu	Asp	Val	Asn	Asp	Asn	Thr	Pro	Ala	Ile	Thr	Ile	Thr	Pro	Leu	Thr
			340					345					350		
Thr	Val	Asn	Ala	Gly	Val	Ala	Tyr	Ile	Pro	Glu	Thr	Ala	Thr	Lys	Glu
		355					360					365			
Asn	Phe	Ile	Ala	Leu	Ile	Ser	Thr	Thr	Asp	Arg	Ala	Ser	Gly	Ser	Asn
	370					375					380				

000031-031104
FOI 201-031104

Gly	Gln	Val	Arg	Cys	Thr	Leu	Tyr	Gly	His	Glu	His	Phe	Lys	Leu	Gln	385	390	395	400
Gln	Ala	Tyr	Glu	Asp	Ser	Tyr	Met	Ile	Val	Thr	Thr	Ser	Thr	Leu	Asp	405	410	415	
Arg	Glu	Asn	Ile	Ala	Ala	Tyr	Ser	Leu	Thr	Val	Val	Ala	Glu	Asp	Leu	420	425	430	
Gly	Phe	Pro	Ser	Leu	Lys	Thr	Lys	Lys	Tyr	Tyr	Thr	Val	Lys	Val	Ser	435	440	445	
Asp	Glu	Asn	Asp	Asn	Ala	Pro	Val	Phe	Ser	Lys	Pro	Gln	Tyr	Glu	Ala	450	455	460	
Ser	Ile	Leu	Glu	Asn	Asn	Ala	Pro	Gly	Ser	Tyr	Ile	Thr	Thr	Val	Ile	465	470	475	480
Ala	Arg	Asp	Ser	Asp	Ser	Asp	Gln	Asn	Gly	Lys	Val	Asn	Tyr	Arg	Leu	485	490	495	
Val	Asp	Ala	Lys	Val	Met	Gly	Gln	Ser	Leu	Thr	Thr	Phe	Val	Ser	Leu	500	505	510	
Asp	Ala	Asp	Ser	Gly	Val	Leu	Arg	Ala	Val	Arg	Ser	Leu	Asp	Tyr	Glu	515	520	525	
Lys	Leu	Lys	Gln	Leu	Asp	Phe	Glu	Ile	Glu	Ala	Ala	Asp	Asn	Gly	Ile	530	535	540	
Pro	Gln	Leu	Ser	Thr	Arg	Val	Gln	Leu	Asn	Leu	Arg	Ile	Val	Asp	Gln	545	550	555	560
Asn	Asp	Asn	Cys	Pro	Val	Ile	Thr	Asn	Pro	Leu	Leu	Asn	Asn	Gly	Ser	565	570	575	
Gly	Glu	Val	Leu	Leu	Pro	Ile	Ser	Ala	Pro	Gln	Asn	Tyr	Leu	Val	Phe	580	585	590	
Gln	Leu	Lys	Ala	Glu	Asp	Ser	Asp	Glu	Gly	His	Asn	Ser	Gln	Leu	Phe	595	600	605	
Tyr	Thr	Ile	Leu	Arg	Asp	Pro	Ser	Arg	Leu	Phe	Ala	Ile	Asn	Lys	Glu	610	615	620	
Ser	Gly	Glu	Val	Phe	Leu	Lys	Lys	Gln	Leu	Asn	Ser	Asp	His	Ser	Glu	625	630	635	640
Asp	Leu	Ser	Ile	Val	Val	Ala	Val	Tyr	Asp	Leu	Gly	Arg	Pro	Ser	Leu	645	650	655	

Ser	Thr	Asn	Ala	Thr	Val	Lys	Phe	Ile	Leu	Thr	Asp	Ser	Phe	Pro	Ser		
			660					665					670				
Asn	Val	Glu	Val	Val	Ile	Leu	Gln	Pro	Ser	Ala	Glu	Glu	Gln	His	Gln		
		675					680					685					
Ile	Asp	Met	Ser	Ile	Ile	Phe	Ile	Ala	Val	Leu	Ala	Gly	Gly	Cys	Ala		
	690					695					700						
Leu	Leu	Leu	Leu	Ala	Ile	Phe	Phe	Val	Ala	Cys	Thr	Cys	Lys	Lys	Lys		
705					710					715					720		
Ala	Gly	Glu	Phe	Lys	Gln	Val	Pro	Glu	Gln	His	Gly	Thr	Cys	Asn	Glu		
				725					730					735			
Glu	Arg	Leu	Leu	Ser	Thr	Pro	Ser	Pro	Gln	Ser	Val	Ser	Ser	Ser	Leu		
		740						745					750				
Ser	Gln	Ser	Glu	Ser	Cys	Gln	Leu	Ser	Ile	Asn	Thr	Glu	Ser	Glu	Asn		
		755					760					765					
Cys	Ser	Val	Ser	Ser	Asn	Gln	Glu	Gln	His	Gln	Gln	Thr	Gly	Ile	Lys		
	770					775					780						
His	Ser	Ile	Ser	Val	Pro	Ser	Tyr	His	Thr	Ser	Gly	Trp	His	Leu	Asp		
785					790					795					800		
Asn	Cys	Ala	Met	Ser	Ile	Ser	Gly	His	Ser	His	Met	Gly	His	Ile	Ser		
			805						810					815			
Thr	Lys	Asp	Ser	Gly	Lys	Gly	Asp	Ser	Asp	Phe	Asn	Asp	Ser	Asp	Ser		
			820					825					830				
Asp	Thr	Ser	Gly	Glu	Ser	Gln	Lys	Lys	Ser	Ile	Glu	Gln	Pro	Met	Gln		
		835					840					845					
Ala	Gln	Ala	Ser	Ala	Gln	Tyr	Thr	Asp	Glu	Ser	Ala	Gly	Phe	Arg	His		
	850					855					860						
Ala	Asp	Asn	Tyr	Phe	Ser	His	Arg	Ile	Asn	Lys	Gly	Pro	Glu	Asn	Gly		
865					870					875					880		
Asn	Cys	Thr	Leu	Gln	Tyr	Glu	Lys	Gly	Tyr	Arg	Leu	Ser	Tyr	Ser	Val		
			885						890					895			
Ala	Pro	Ala	His	Tyr	Asn	Thr	Tyr	His	Ala	Arg	Met	Pro	Asn	Leu	His		
			900					905					910				
Ile	Pro	Asn	His	Thr	Leu	Arg	Asp	Pro	Tyr	Tyr	His	Ile	Asn	Asn	Pro		
		915					920					925					

Val Ala Asn Arg Met His Ala Glu Tyr Glu Arg Asp Leu Val Asn Arg
 930 935 940

Ser Ala Thr Leu Ser Pro Gln Arg Ser Ser Ser Arg Tyr Gln Glu Phe
 945 950 955 960

Asn Tyr Ser Pro Gln Ile Ser Arg Gln Leu His Pro Ser Glu Ile Ala
 965 970 975

Thr Thr Phe

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATCCCCAG AGATGAACTC CTTGAGATTG TTTTAAATGA CTGCAGGTCT GGAAGGATTC	60
ACATTGCCAC ACTGTTTCTA GGCATGAAAA AACTGCAAGT TTCAACTTTG TTTTGGGTGC	120
AACTTTGATT CTTCAAGATG CTGCTTCTCT TCAGAGCCAT TCCAATGCTG CTGTTGGGAC	180
TGATGGTTTT ACAACAGAC TGTGAAATTG CCCAGTACTA CATAGATGAA GAAGAACCCC	240
CTGGCACTGT AATTGCAGTG TTGTCACAAC ACTCCATATT TAACACTACA GATATACCTG	300
CAACCAATTT CCGTCTAATG AAGCAATTTA ATAATTCCCT TATCGGAGTC CGTGAGAGTG	360
ATGGGCAGCT GAGCATCATG GAGAGGATTG ACCGGGAGCA AATCTGCAGG CAGTCCCTTC	420
ACTGCAACCT GGCTTTGGAT GTGGTCAGCT TTTCCAAAGG AACTTCAAG CTTCTGAACG	480
TGAAAGTGGG GGTGAGAGAC ATTAATGACC ATAGCCCTCA CTTTCCAGT GAAATAATGC	540
ATGTGGAGGT GTCTGAAAGT TCCTCTGTGG GCACCAGGAT TCCTTTAGAA ATTGCAATAG	600
ATGAAGATGT TGGGTCCAAC TCCATCCAGA ACTTTCAGAT CTCAAATAAT AGCCACTTCA	660
GCATTGATGT GCTAACCAGA GCAGATGGGG TGAAATATGC AGATTTAGTC TTAATGAGAG	720
AACTGGACAG GGAAATCCAG CCAACATACA TAATGGAGCT ACTAGCAATG GATGGGGGTG	780

ATGAAGAACG CCTGTTAAGC ACCCCATCTC CCCAGTCGGT CTCTTCTTCT TTGTCTCAGT	2400
CTGAGTCATG CCAACTCTCC ATCAATACTG AATCTGAGAA TTGCAGCGTG TCCTCTAACC	2460
AAGAGCAGCA TCAGCAAACA GGCATAAAGC ACTCCATCTC TGTACCATCT TATCACACAT	2520
CTGGTTGGCA CCTGGACAAT TGTGCAATGA GCATAAGTGG ACATTCTCAC ATGGGGCACA	2580
TTAGTACAAA GGACAGTGGC AAAGGAGATA GTGACTTCAA TGACAGTGAC TCTGATACTA	2640
GTGGAGAATC ACAAAGAAG AGCATTGAGC AGCCAATGCA GGCACAAGCC AGTGCTCAAT	2700
ACACAGATGA ATCAGCAGGG TTCCGACATG CCGATAACTA TTTCAGCCAC CGAATCAACA	2760
AGGGTCCAGA AAATGGGAAC TGCACATTGC AATATGAAAA GGGCTATAGA CTGTCTTACT	2820
CTGTAGCTCC TGCTCATTAC AATACCTACC ATGCAAGAAT GCCTAACCTG CACATACCGA	2880
ACCATACCCT TAGAGACCCT TATTACCATA TCAATAATCC TGTGCTAAT CGGATGCACG	2940
CGGAATATGA AAGAGATTTA GTCAACAGAA GTGCAACGTT ATCTCCGCAG AGATCGTCTA	3000
GCAGATACCA AGAATTCAAT TACAGTCCGC AGATATCAAG ACAGCTTCAT CCTTCAGAAA	3060
TTGCTACAAC CTTTTAATCA TTAGGCATGC AAGTGAGAAT GCACAAAGGC AAGTGCTTTA	3120
GCATGAAAGC TAAATATATG GAGTCTCCCC TTTCCCTCTG ATGGATGGGG GGAGACACAG	3180
GACAGTGCAT AAATATACAG CTGCTTTCTA TTTGCATTTT ACTTGGAAT TTTTGTGTTT	3240
TTTTACATAT TTATTTTCC TGAATTGAAT GTGACATTGT CCTGTCACCT AACTAGCAAT	3300
TAAATCCACA GACCTACAGT CAAATATTG AGGGCCCCTG AAACAGCACA TCAGTCAGGA	3360
CCTAAAGTGG CCTTTTTACT TTTAGCAGCT CCTGGGTCTG CCCTCTGTGT TAATCAGCCC	3420
CTGGTCAAGT CCTGAGTAGG ATCATGGCGT TTTTATATGC ATCTCACCTA CTTTGGACGT	3480
GATTACACA TAATAGGAAA CGCTTGTTT CAGTGAAGTC TGTGTTGTAT ATATTCTGTT	3540
ATATACACGC ATTTTGTGTT TGTGTATATA TTTCAAGTCC ATTCAGATAT GTGTATATAG	3600
TGCAGACCTT GTAAATTAAA TATTCTGATA CTTTTTCCTC AATAAATATT TAAAT	3655

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Val Cys Cys Gly Pro Gly Arg Met Leu Leu Gly Trp Ala Gly Leu
1 5 10 15
Leu Val Leu Ala Ala Leu Cys Leu Leu Gln Val Pro Gly Ala Gln Ala
20 25 30
Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys Ser Leu Pro Trp
35 40 45
Asn Met Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Ala Asn
50 55 60
Ala Ile Leu Ala Met Glu Gln Phe Glu Gly Leu Leu Gly Thr His Cys
65 70 75 80
Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys
85 90 95
Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys
100 105 110
Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His
115 120 125
Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu Pro Val Tyr Asp Arg
130 135 140
Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp
145 150 155 160
Phe Pro Met Asp Ser Ser Thr Gly His Cys Arg Gly Ala Ser Ser Glu
165 170 175
Arg Cys Lys Cys Lys Pro Val Arg Ala Thr Gln Lys Thr Tyr Phe Arg
180 185 190
Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Val Lys Met
195 200 205
Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys
210 215 220
Ala Ser Leu Val Asn Ile Pro Arg Asp Thr Val Asn Leu Tyr Thr Thr
225 230 235 240

Ser Gly Cys Leu Cys Pro Pro Leu Thr Val Asn Glu Glu Tyr Val Ile
 245 250 255

Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
 260 265 270

Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
 275 280 285

Trp Asp Met Lys Leu Arg His Leu Gly Leu Gly Lys Thr Asp Ala Ser
 290 295 300

Asp Ser Thr Gln Asn Gln Lys Ser Gly Arg Asn Ser Asn Pro Arg Pro
 305 310 315 320

Ala Arg Ser

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AAGCCTGGGA CCATGGTCTG CTGCGGCCCG GGACGGATGC TGCTAGGATG GGCCGGGTTG	60
CTAGTCCTGG CTGCTCTCTG CCTGCTCCAG GTGCCCGGAG CTCAGGCTGC AGCCTGTGAG	120
CCTGTCCGCA TCCCGCTGTG CAAGTCCCTT CCCTGGAACA TGACCAAGAT GCCCAACCAC	180
CTGCACCACA GCACCCAGGC TAACGCCATC CTGGCCATGG AACAGTTCGA AGGGCTGCTG	240
GGCACCCACT GCAGCCCGGA TCTTCTCTTC TTCCTCTGTG CAATGTACGC ACCCATTTGC	300
ACCATCGACT TCCAGCACGA GCCCATCAAG CCCTGCAAGT CTGTGTGTGA GCGCGCCCGA	360
CAGGGCTGCG AGCCCATTCT CATCAAGTAC CGCCACTCGT GGCCGGAAAG CTTGGCCTGC	420
GACGAGCTGC CGGTGTACGA CCGCGGCGTG TGCATCTCTC CTGAGGCCAT CGTCACCGCG	480
GACGGAGCGG ATTTTCCTAT GGATTCAAGT ACTGGACACT GCAGAGGGGC AAGCAGCGAA	540
CGTTGCAAAT GTAAGCCTGT CAGAGCTACA CAGAAGACCT ATTTCCGGAA CAATTACAAC	600

TTGTGTTGTT TAATGCTCCA TCAAGATGTC TAATAAAAGG AATATGGTTG TCAACAGAGA 2160
CGACAACAAC AACAAA 2176

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Val Cys Gly Ser Pro Gly Gly Met Leu Leu Leu Arg Ala Gly Leu
1 5 10 15
Leu Ala Leu Ala Ala Leu Cys Leu Leu Arg Val Pro Gly Ala Arg Ala
20 25 30
Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys Ser Leu Pro Trp
35 40 45
Asn Met Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Ala Asn
50 55 60
Ala Ile Leu Ala Ile Glu Gln Phe Glu Gly Leu Leu Gly Thr His Cys
65 70 75 80
Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys
85 90 95
Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys
100 105 110
Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His
115 120 125
Ser Trp Pro Glu Asn Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg
130 135 140
Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp
145 150 155 160
Phe Pro Met Asp Ser Ser Asn Gly Asn Cys Arg Gly Ala Ser Ser Glu
165 170 175

Arg Cys Lys Cys Lys Pro Ile Arg Ala Thr Gln Lys Thr Tyr Phe Arg
 180 185 190
 Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Ile Lys Thr
 195 200 205
 Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys
 210 215 220
 Ser Ser Leu Val Asn Ile Pro Arg Asp Thr Val Asn Leu Tyr Thr Ser
 225 230 235 240
 Ser Gly Cys Leu Cys Pro Pro Leu Asn Val Asn Glu Glu Tyr Ile Ile
 245 250 255
 Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
 260 265 270
 Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
 275 280 285
 Trp Asp Met Lys Leu Arg His Leu Gly Leu Ser Lys Ser Asp Ser Ser
 290 295 300
 Asn Ser Asp Ser Thr Gln Ser Gln Lys Ser Gly Arg Asn Ser Asn Pro
 305 310 315 320
 Arg Gln Ala Arg Asn
 325

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1893 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGCGGAGCGG GCCTTTTGGC GTCCACTGCG CGGCTGCACC CTGCCCCATC TGCCGGGATC	60
ATGGTCTGCG GCAGCCCGGG AGGGATGCTG CTGCTGCGGG CCGGGCTGCT TGCCCTGGCT	120
GCTCTCTGCC TGCTCCGGGT GCCCGGGGCT CGGGCTGCAG CCTGTGAGCC CGTCCGCATC	180
CCCCTGTGCA AGTCCCTGCC CTGGAACATG ACTAAGATGC CCAACCACCT GCACCACAGC	240

ACTCAGGCCA	ACGCCATCCT	GGCCATCGAG	CAGTTCGAAG	GTCTGCTGGG	CACCCACTGC	300
AGCCCCGATC	TGCTCTTCTT	CCTCTGTGCC	ATGTACGCGC	CCATCTGCAC	CATTGACTTC	360
CAGCACGAGC	CCATCAAGCC	CTGTAAGTCT	GTGTGCGAGC	GGGCCCCGCA	GGGCTGTGAG	420
CCCATACTCA	TCAAGTACCG	CCACTCGTGG	CCGGAGAACC	TGGCCTGCGA	GGAGCTGCCA	480
GTGTACGACA	GGGGCGTGTG	CATCTCTCCC	GAGGCCATCG	TTACTGCGGA	CGGAGCTGAT	540
TTTCCTATGG	ATTCTAGTAA	CGGAAACTGT	AGAGGGGCAA	GCAGTGAACG	CTGTAAATGT	600
AAGCCTATTA	GAGCTACACA	GAAGACCTAT	TTCCGGAACA	ATTACAATA	TGTCATTCGG	660
GCTAAAGTTA	AAGAGATAAA	GACTAAGTGC	CATGATGTGA	CTGCAGTAGT	GGAGGTGAAG	720
GAGATTCTAA	AGTCCTCTCT	GGTAAACATT	CCACGGGACA	CTGTCAACCT	CTATACCAGC	780
TCTGGCTGCC	TCTGCCCTCC	ACTTAATGTT	AATGAGGAAT	ATATCATCAT	GGGCTATGAA	840
GATGAGGAAC	GTTCCAGATT	ACTCTTGGTG	GAAGGCTCTA	TAGCTGAGAA	GTGGAAGGAT	900
CGACTCGGTA	AAAAAGTTAA	GCGCTGGGAT	ATGAAGCTTC	GTCATCTTGG	ACTCAGTAAA	960
AGTGATTCTA	GCAATAGTGA	TTCCACTCAG	AGTCAGAAGT	CTGGCAGGAA	CTCGAACCCC	1020
CGGCAAGCAC	GCAACTAAAT	CCCGAAATAC	AAAAAGTAAC	ACAGTGGACT	TCCTATTAAG	1080
ACTTACTTGC	ATTGCTGGAC	TAGCAAAGGA	AAATTGCACT	ATTGCACATC	ATATTCTATT	1140
GTTTACTATA	AAAATCATGT	GATAACTGAT	TATTACTTCT	GTTTCTCTTT	TGGTTTCTGC	1200
TTCTCTCTTC	TCTCAACCCC	TTTGTAATGG	TTTGGGGGCA	GACTCTTAAG	TATATTGTGA	1260
GTTTTCTATT	TCACTAATCA	TGAGAAAAAC	TGTTCTTTTG	CAATAATAAT	AAATTAAACA	1320
TGCTGTTACC	AGAGCCTCTT	TGCTGAGTCT	CCAGATGTTA	ATTTACTTTC	TGCACCCCAA	1380
TTGGGAATGC	AATATTGGAT	GAAAAGAGAG	GTTTCTGGTA	TTCACAGAAA	GCTAGATATG	1440
CCTTAAACA	TACTCTGCCG	ATCTAATTAC	AGCCTTATTT	TTGTATGCCT	TTTGGGCATT	1500
CTCCTCATGC	TTAGAAAGTT	CCAAATGTTT	ATAAAGGTAA	AATGGCAGTT	TGAAGTCAAA	1560
TGTCACATAG	GCAAAGCAAT	CAAGCACCAG	GAAGTGTTTA	TGAGGAAACA	ACACCCAAGA	1620
TGAATTATTT	TTGAGACTGT	CAGGAAGTAA	AATAAATAGG	AGCTTAAGAA	AGAACATTTT	1680
GCCTGATTGA	GAAGCACAAC	TGAAACCAGT	AGCCGCTGGG	GTGTTAATGG	TAGCATTCTT	1740
CTTTTGCCAA	TACATTTGAT	TTGTTTCATGA	ATATATTAAT	CAGCATTAGA	GAAATGAATT	1800

ATAACTAGAC ATCTGCTGTT ATCACCATAG TTTTGTTTAA TTTGCTTCCT TTAAATAAA 1860

CCCATTGGTG AAAGTCAAAA AAAAAAAAAA AAA 1893

FOR THE RECORD